

FIGURE 1

GAGCTCGGAT CCACTACTCG ACCCACCGGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG	60
CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA	120
TCGCGGAGCA GGGGCCCGA ACTCCGGCG CGCGGCC ATG CGC CGG GCC AGC CGA Met Arg Arg Ala Ser Arg	175
1 5	
GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro	223
10 15 20	
GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala	271
25 30 35	
CCG GCG CCG CCA CCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG Pro Ala Pro Pro Ala Ala Ser Arg Ser <u>Met Phe</u> Leu Ala <u>Leu Leu</u>	319
40 45 50	
GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC <u>Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr</u>	367
55 60 65 70	
TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His	415
75 80 85	
TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp	463
90 95 100	
TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met	511
105 110 115	
AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val	559
120 125 130	
GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp	607
135 140 145 150	
TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His	655
155 160 165	
CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr	703
170 175 180	

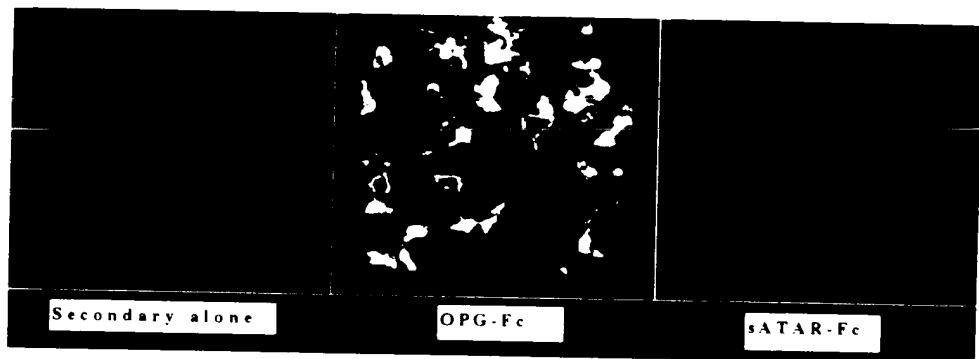
FIGURE 1 (Con't)

ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr 200 205 210	799
CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCC CGA ACC CTA Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val 215 220 225 230	847
CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile 235 240 245	895
AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Ser Thr Lys <u>Asn</u> 250 255 260	943
TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly 265 270 275	991
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser <u>Asn</u> 280 285 290	1039
CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe 295 300 305 310	1087
AAA GTT CAG GAC ATA GAC T GAGACTCATT TCGTGGAAACA TTAGCATGGA Lys Val Gln Asp Ile Asp 315	1136
TGTCCTAGAT GTTTGGAAAC TTCTTAAAAA ATGGATGATG TCTATACATG TGTAAGACTA	1196
CTAAGAGACA TGGCCCACGG TGTATGAAAC TCACAGCCCT CTCTCTTGAG CCTGTACAGG	1256
TGTGTATAT GTAAAGTCCA TAGGTGATGT TAGATTCATG GTGATTACAC AACGGTTTA	1316
CAATTTGTA ATGATTCCT AGAATTGAAC CAGATTGGA GAGGTATTCC GATGCTTATG	1376
AAAAACTTAC ACGTGAGCTA TGGAGGGGG TCACTAGTCAC TGGGTCTAAC CCTGGACAT	1436
GTGCCACTGA GAACCTTGAA ATTAAGAGGA TGGCATGTCA TGGAAAGAA ATGATAGTGT	1496
GAAGGGTTAA GTTCTTTGA ATTGTTACAT TGCCTGGGA CCTGCAAATA AGTCTTTT	1556
TTCTAATGAG GAGAGAAAAA TATATGTATT TTTATATAAT GTCTAAAGTT ATATTCAGG	1616
TGAAATGTT TCTGTGCAA GTTTTGTAAA TTATATTGT GCTATAGTAT TTGATTCAA	1676

**FIGURE 1 (Con't)**

TCAAAACTAT GCAAGCAAAA TAAATAAATA AAAATAAAAT GAATACCTTG AATAATAAGT	1916
AGGATGTTGG TCACCCAGGTG CCTTTCAAAT TTAGAAGCTA ATTGACTTTA GGAGCTGACA	1976
TAGCCAAAAA GGATACATAA TAGGCTACTG AAATCTGTCA GGAGTATTAA TCCAATTATT	2036
GAACAGGTGT CTTTTTTAC AAGAGCTACA AATTGTAAAT TTTGTTCTT TTTTTTCCCA	2096
TAGAAAATGT ACTATAGTTT ATCAGCCAAA AAACAATCCA CTTTTAATT TAGTGAAAGT	2156
TATTTTATTA TACTGTACAA TAAAAGCATT GTCTCTGAAT GTTAATTTT TGGTACAAAA	2216
AATAAATTG TACGAAAACC TGAAAAAAAAA AAAAAAAAAA AAAAAAAGGG CGGCCGCTCT	2276
AGAGGGCCCT ATTCTATAG	2295

Expression of 32D-F3 in COS-7 Cells



...JHE

## OPG Binding Protein Expression in Human Tissues

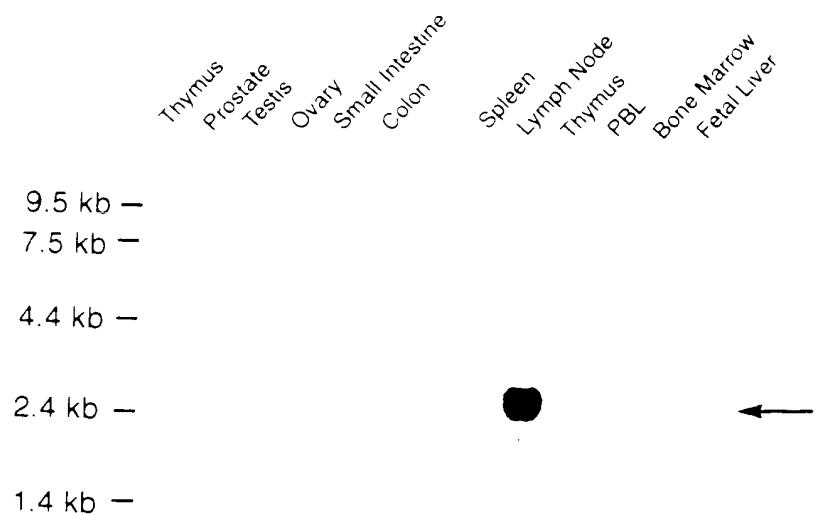


FIGURE 3

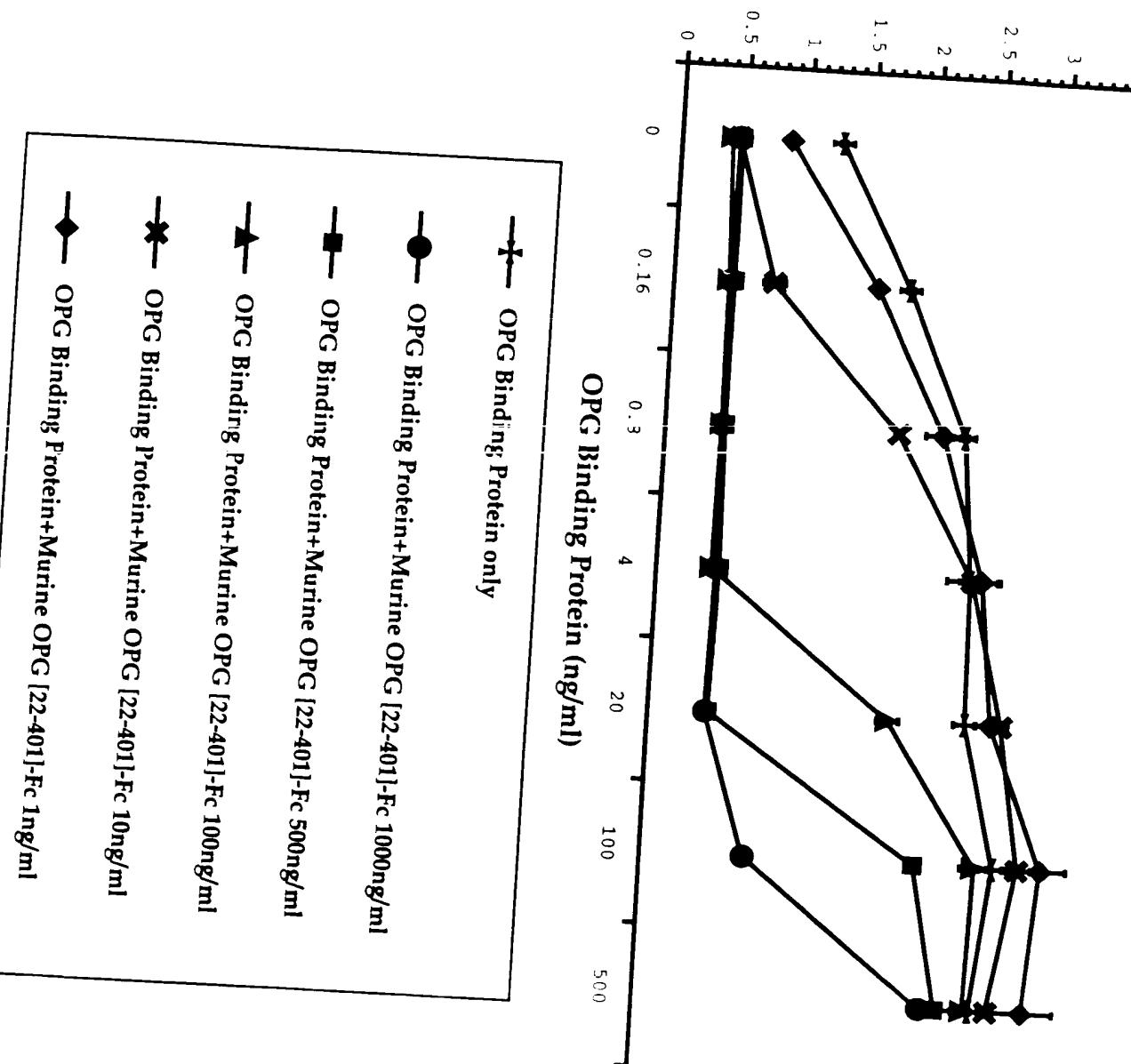
FIGURE 4

320 330 340  
 AAGGTTGGTACCGAGCTGGATCACTACTGGAUCCACGGCTCCGGCGCCCCAAGGAGC  
 350 360 370  
 AAAGCCGGGCTCAAGTCGGCGCCCCACGGTGGAGCTCCGGCGAGCTCCGGATTCGG  
 380 390 400  
 CCCAGACAAAGAAGGGAGGGAGGGAGGGAGGAAGCTCCAAAGGAGAGGGGGAG  
 410 420 430  
 CGCCATGC CGCG CCGAGGAGAGACTACAGCTTACCTGGCTTCCTGCGCGATCGG  
 M R R A S R D F T K Y L R G S E E M G  
 440 450 460  
 CGGCGGCCCGGA CGCCCGGACGGAG CGCGCTCTGCATGCCCGCGCGCGCGCG  
 G G F G A P H E S P L H A P P P P A P H  
 470 480 490  
 CCAGCCCGCCCGCTCCCGCTCCATGTTGGCTCCCTGCGGCTGGGTGGCGCA  
 Q P P A A S R S M F V A L L G L G L G Q  
 500 510 520  
 CGITGCTCGCACCGCTCGCCCTGTTCCTTCATTTCAAGAGCCAGATGGATCTAAATAGAAT  
 V V C S V A L F F Y F R A Q M D P H E I  
 530 540 550  
 ATCAGAAGATGGCACTCACTGCATTCATAGAAATTGAGACTCCATGAAAATGGAGATTT  
 S S D G T H C I Y R I L E L H M A I F  
 560 570 580  
 TCAAGACACAACTCTGGAGAGTCAAGATAAAATTAAATACCTGATTCAAGTAGGAGAAT  
 Q D T T I E S Q D T K L I P D S C R R I  
 590 600 610  
 TAAACAGGCCCTTCAGGAGCTGTGCAAAAGGAATTACAACATATCGTGTGATCACACCCA  
 K Q A F Q G A V Q F E L Q H I V G S Q R  
 620 630 640  
 CATCAGAGAGAAAGCGATGGGGATGCTCATGGTAGATCTGGCCAAGAGGAGCAA  
 I R A E K A M V D G S W L D L A F R S K  
 650 660 670  
 GCTTGAAGCTAGCCTTTGCTCATCTCATTTAATGCCACCGACATCCCATCTGGTC  
 L E A Q P F A H L T I N A T D I P S G S  
 680 690 700  
 CCATAAAAGTGAGTCTGCTCTGGTACCATGATCGGGGTTGGCCAAGATCTCAACAT  
 H K V S L S S W Y H D R G W A K I S N M  
 710 720 730  
 GACTTTAGCAATGAAAATCAATAGTAATCAGGATGGCTTTATTACCTGTATGCCAA  
 T F S N G E L I V N Q D G F Y Y L Y A N  
 740 750 760  
 CATTTGCTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATTTCAACTAAT  
 I C F E H H E T S G D L A T E Y I Q L M  
 770 780 790  
 GGTGTACGTCACTAAACAGCATCAAAATGCCAAGTCTCATACCGCTGATGAAAGGAGG  
 V Y V T K T S I K I P S S H T L M K G G  
 800 810 820  
 AAGGACCAAGTAATGCTGGGAACTCTGGATTCAGGATTTTCTGCTGATGTTGCTG  
 S T F Y M S V N R P H T V H I P I N P I  
 830 840 850  
 ATTTTGAAAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA  
 F F F I P H G I H I H I P I N N P R I  
 860 870 880  
 GGATCGGGATCAAGATGACACATACCTGGGCTCTTAAAGTTGGAGATGAGATTGGAG  
 D P D Q D A T Y F G A F R V R D I D  
 890 900 910  
 CCCAGTTTTGTTGTTATGATTTGTTGTTGTTGAAATTTTTTAAAGGAG  
 920 930 940  
 AAGAGATGATGATATAAATGTTGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAA

FIGURE 4 (Con't)

1391 1411 1431  
CCAGATTGGCAATTACGGGTTGACCTTATGAGAAACTGCATGTGGGGTATGGGAGGG  
1451 1471 1491  
TTGTCCTGGTCATGTGGCCCTTUGCAGCTGAACTGGAGAGGGTGTCACTAGGGCAAT  
1511 1531 1551  
TGAAGGATCATCTGAACGGGCAAATTCTTTCGAAATTGTTACATCATGCTGGAACCTGCAA  
1570 1590 1610  
AAAATACCTTCTTAATGAGGAGAGAAAATATATGTATTTTATATAATATCTAAAGTTA  
1630 1650 1670  
TATTTCAAGATGTAATGTTTCCTTGCAAACTATTGTAAATTATTTGTGCTATAGTATT  
1690 1710 1730  
TGATTCAAAATATTTAAAAATGCTCTTGCTGTTGACATATTAAATGTTTAAATGTACAGA  
1750 1770 1790  
CATATTAACTGGTGCACCTTGAAATTGCTGGGAAACTTGCAAGCTAAGGAGGGAA  
1810 1830 1850  
AAAAATGTTGTTCCCTAATATCAAATGCAAGTATATTTCCTCGTTCTTTAAAGTTAATAG  
1870 1890 1910  
ATTTTTCAAGACTTGTCAAGCCTGTGCAAAAAAATTAAAATGGATGCCTTGAATAATAAG  
1930 1950 1970  
CAGGATGTTGCCACCAAGGTGCCTTCAAAATTAGAAACTAAATTGACTTTAGAAAGCTGA  
1990 2010 2030  
CATTGCCAAAAGGATACATAATGGCCACTGAAATCTGTCAAGAGTAGTTATATAATTG  
2050 2070 2090  
TTCAACACCTTTTCCACAAGTGGCGAAATTGTACCTTTTTTCAAAATAG  
2110 2130 2150  
AAAAGTTATTAAGTGGTTATCAGGAAAAAGTCCAATTAAATTAGTAAATGTTATCTT  
2170 2190 2210  
ATACTGTACAATAAAAACATTGCCTTGAATGTTAATTGGTACAAAAATAATTAA  
2230 2250 2270  
TATGAAAAAAGGGCGCCGCTAGAGGCCCTATTCTATAG

A405



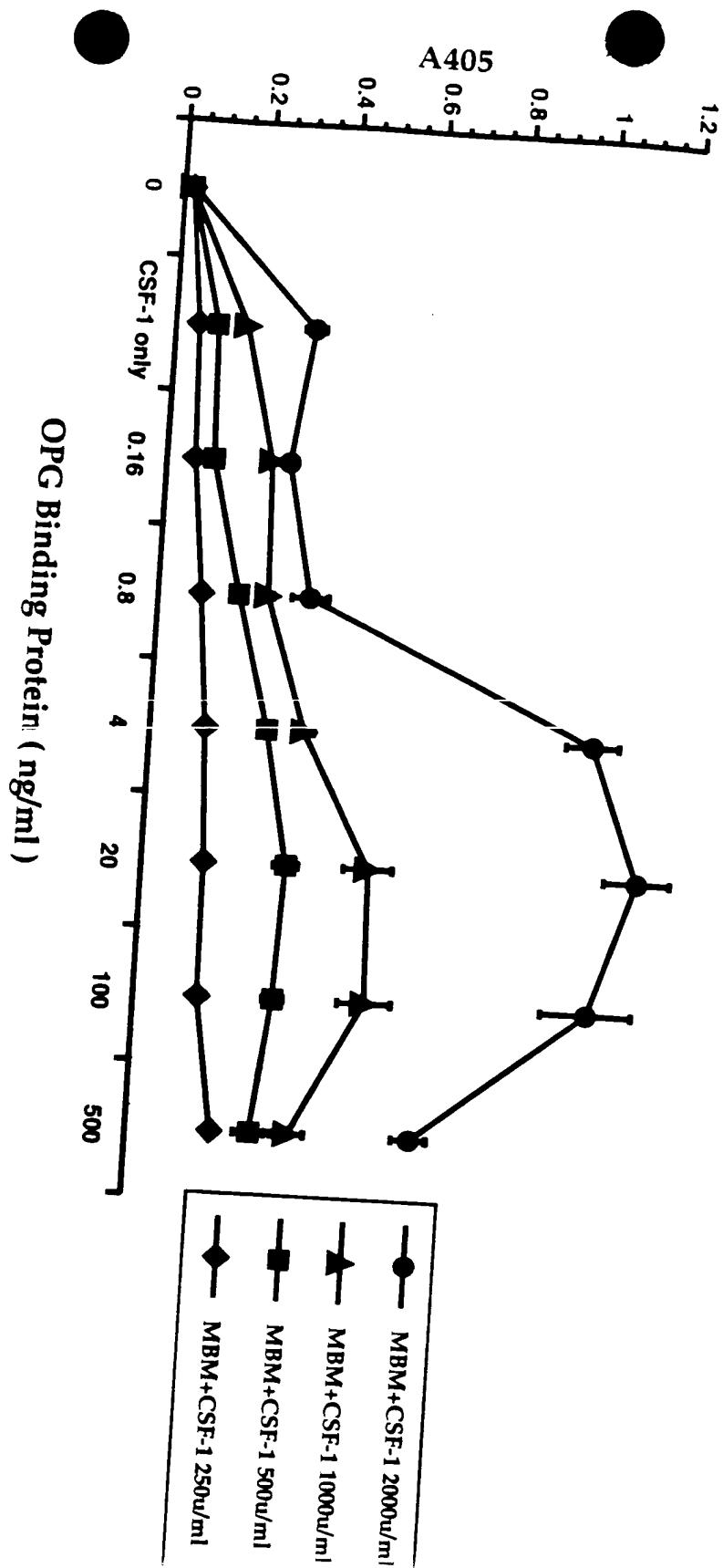
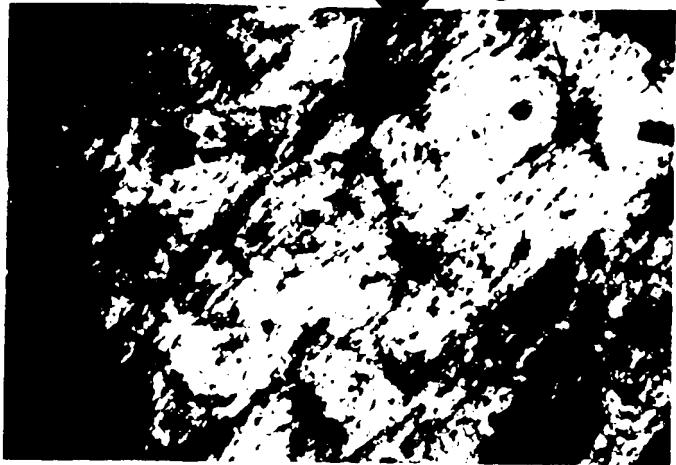


FIGURE 6

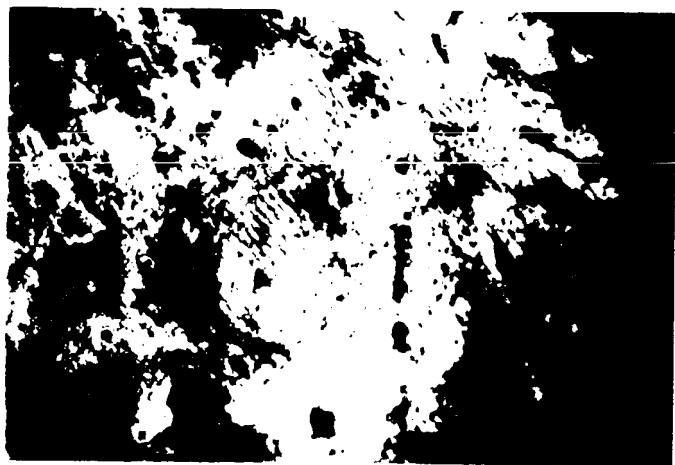
Toluidine Blue staining



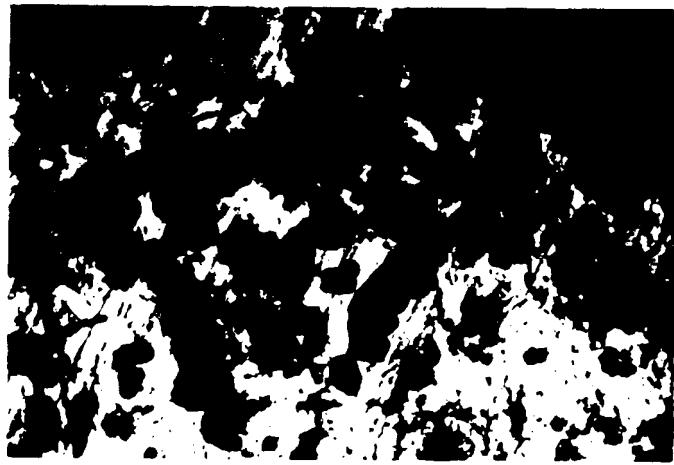
Toluidine Blue staining



Bone Marrow Cells + M-CSF-1



Bone Marrow Cells + OPG Binding Protein



Bone Marrow Cells + M-CSF-1 +OPG Binding Protein

FIGURE

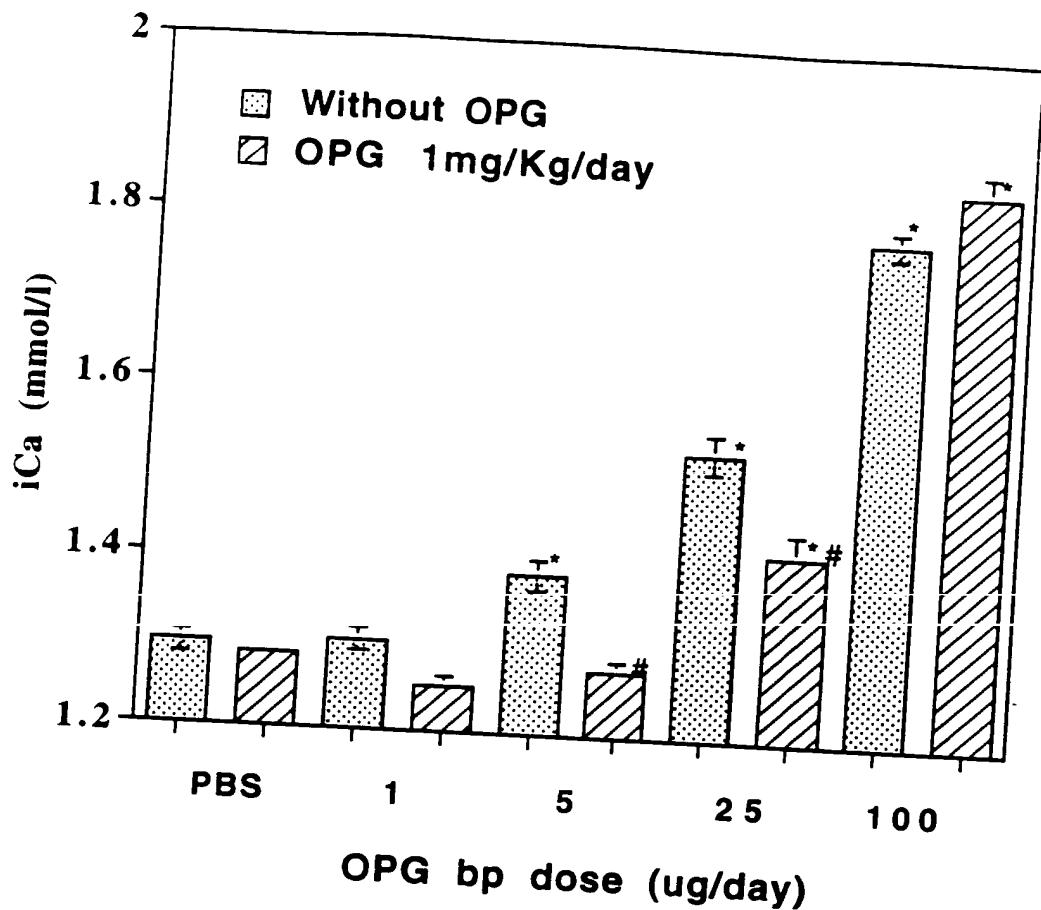


FIGURE 8

**PBS**



**OPGbp 5ug/d**



**OPGbp 25ug/d**



**OPGbp100ug/d**



FIGURE

Figure 10. Murine ODAR cDNA sequence

FIGURE 10

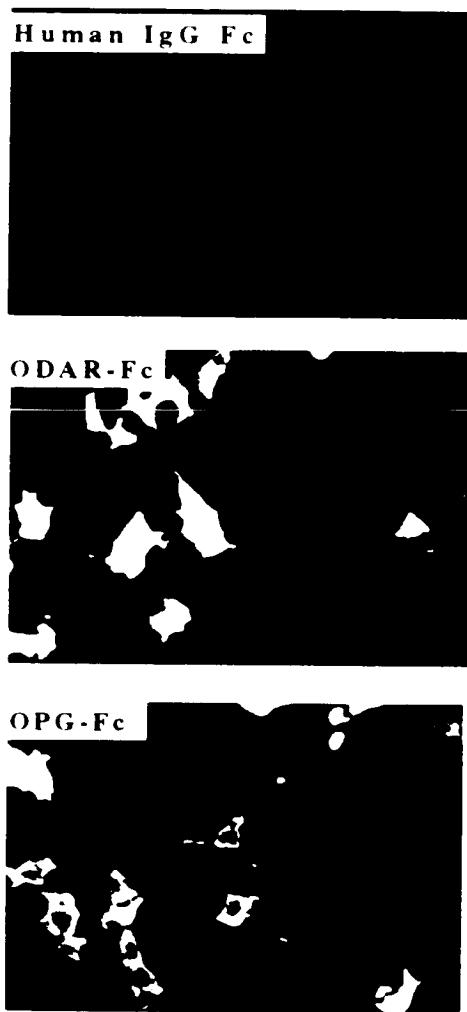


FIGURE 11

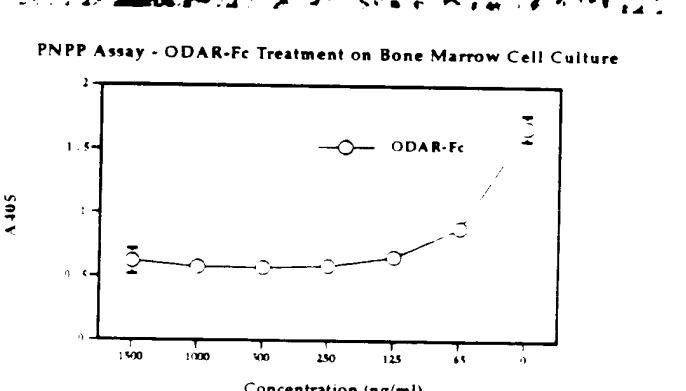
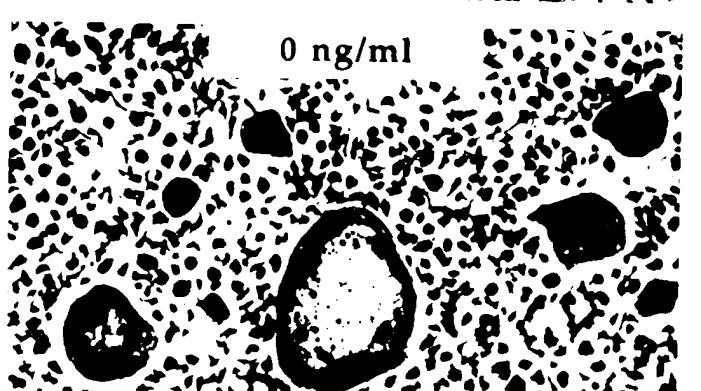
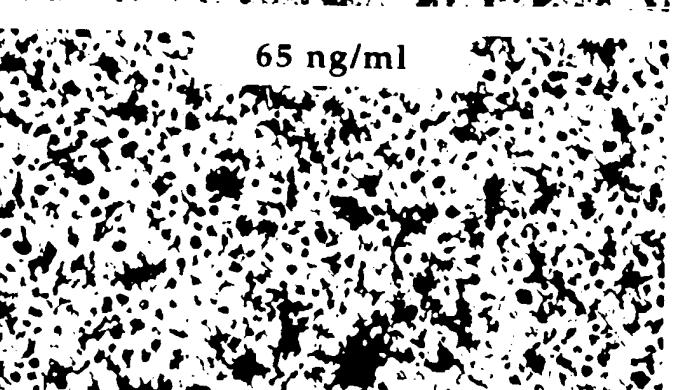
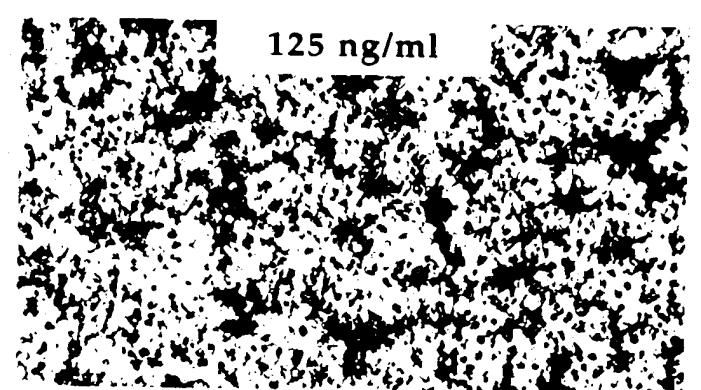
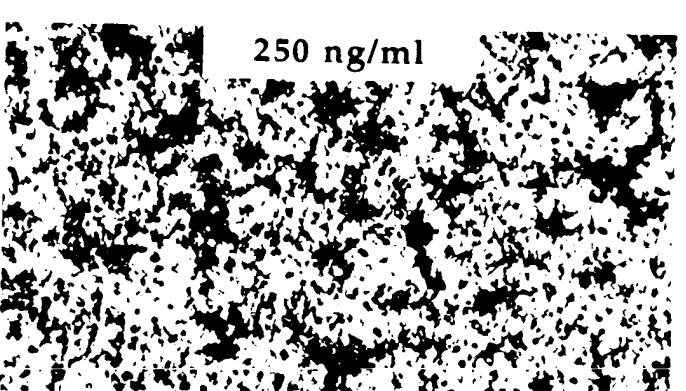
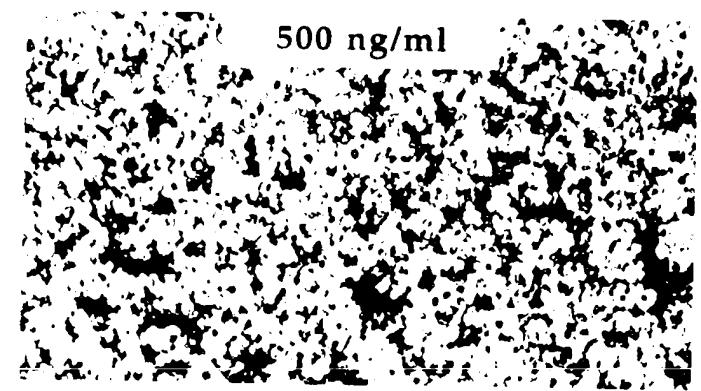
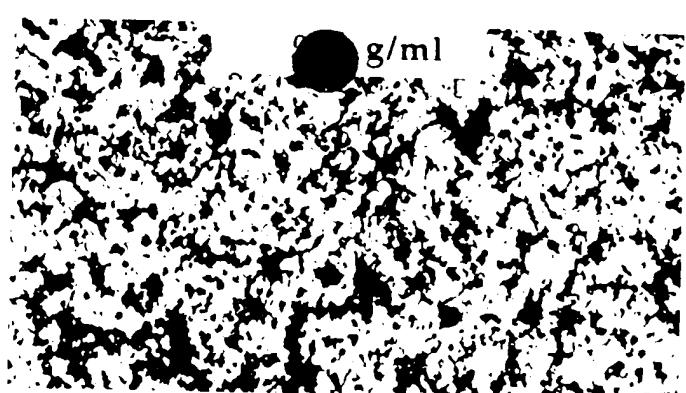
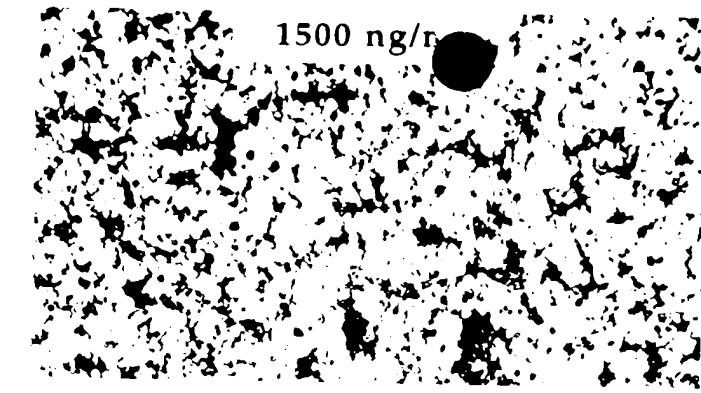
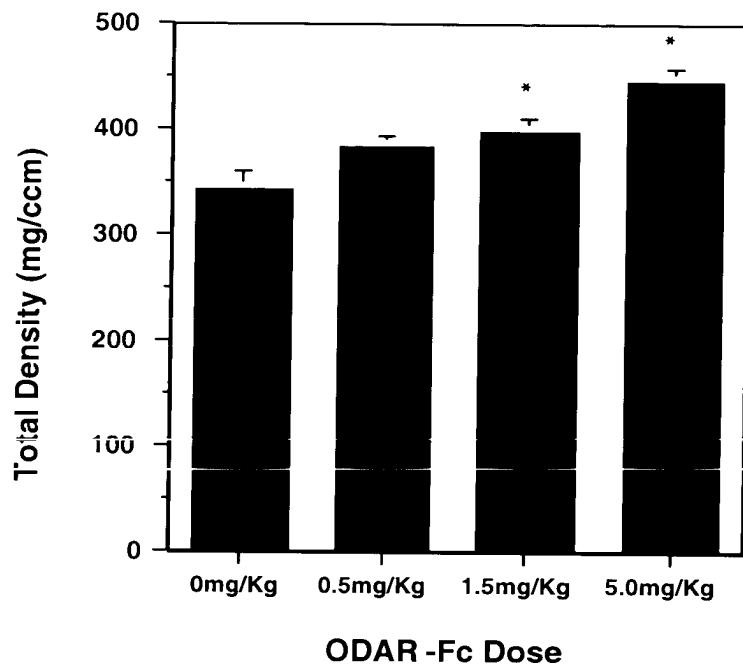


FIGURE 10

FIGURE 13



\* Different to vehicle treated control  $p < 0.05$ .